

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

QM protein - protein search, using sw model

Run on: November 6, 2004, 19:24:00 ; Search time 66.875 Seconds  
(without alignments)  
43.019 Million cell updates/sec

Title: US-10-618-644-5

Perfect score: 27

Sequence: 1 TPRVF 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	48	2	Q41032 pisum sativ
2	27	100.0	51	2	Q8QV41 avian reovi
3	27	100.0	51	2	Q8QV42 avian reovi
4	27	100.0	51	2	Q8QV43 avian reovi
5	27	100.0	51	2	Q8QV46 avian reovi
6	27	100.0	51	2	Q8QV47 avian reovi
7	27	100.0	51	2	Q8QV48 avian reovi
8	27	100.0	51	2	Q8QV51 avian reovi
9	27	100.0	51	2	Q8QV52 avian reovi
10	27	100.0	51	2	Q8QV53 avian reovi
11	27	100.0	51	2	Q8QV55 avian reovi
12	27	100.0	91	2	Q88T47 lactobacill
13	27	100.0	97	2	Q6MNH8 bdellovibri
14	27	100.0	97	2	Cae79173 bdellovib
15	27	100.0	104	2	Q6LHW8 photobacter
16	27	100.0	104	2	C8g23112 photobact
17	27	100.0	108	2	O32358 campylobact
18	27	100.0	114	2	O59363 pyrococcus
19	27	100.0	136	2	Q43672 vicia faba
20	27	100.0	138	2	Q7X116 leptospiril
21	27	100.0	142	2	Q6R05 uncultured
22	27	100.0	142	2	AA519404 unculture
23	27	100.0	159	2	Q8G7W6 bifidobacte
24	27	100.0	167	2	Q9AVD4 nicotiana t
25	27	100.0	174	2	O64683 mesocricetu
26	27	100.0	181	2	Q744N3 mycobacteri
27	27	100.0	181	2	AA502625 mycobacte
28	27	100.0	188	2	Q72S22 leptospira
29	27	100.0	188	2	Q8F318 leptospira
30	27	100.0	188	2	AA569990 leptospir
31	27	100.0	190	2	Q8H7H3 arabidopsis

32 27 100.0 193 2 Q8GBS3 Q8gbe3 treponema m  
33 27 100.0 195 2 Q7U656 Q7u656 synechococc  
34 27 100.0 197 1 ENGB\_ARCFU O28943 archaeoglob  
35 27 100.0 201 2 O54257 O54257 streptomyce  
36 27 100.0 205 2 O52806 O52806 amycolatops  
37 27 100.0 205 2 Q939X4 Q939x4 amycolatops  
38 27 100.0 206 2 Q83WF8 Q83wf8 streptomyce  
39 27 100.0 207 2 Q7XTL9 Q7xtl9 oryza sativ  
40 27 100.0 208 2 Q9HPH0 Q9hph0 halobacteri  
41 27 100.0 237 2 Q8NLI8 Q8nli8 corynebacte  
42 27 100.0 239 2 Q73M68 Q73m68 treponema d  
43 27 100.0 239 2 AAS12158 Aas12158 treponema  
44 27 100.0 244 1 THYX\_PYRAE Q8zwd6 pyrobaculum  
45 27 100.0 247 2 Q89UW7 Q89uw7 bradyrhizob

#### ALIGNMENTS

##### RESULT 1

Q41032 PRELIMINARY; PRT; 48 AA.  
AC Q41032;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Legumin J (Fragment).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87080257; PubMed=2431897;  
RA Brown J.W.S., Feix G., Frendewey D.;  
RT "Accurate in vitro splicing of two pre-mRNA plant introns in a Hela  
cell nuclear extract.";  
RL EMBO J. 5:2749-2758(1986).  
DR EMBL; M26771: AAA33674.1; -.  
DR PIR; T06450; T06450.  
FT NON\_TER 1  
FT NON\_TER 48  
SQ SEQUENCE 48 AA; 5608 MW; 0DAB5FAAF6A7B3D9 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 48;

Best Local Similarity 100.0%; Pred. No. 60; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0;

Qy 1 TPRVF 5

Db 14 TPRVF 18

##### RESULT 2

Q8QV41 PRELIMINARY; PRT; 51 AA.  
AC Q8QV41;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Sigma C protein (Fragment).  
OS Avian reovirus NL119 97M.  
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.  
OX NCBI\_TaxID=177325;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NL119 97M;  
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,  
ter Huurne A.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF354196; AAL83467.1; -.  
DR InterPro; IPR007662; Reo\_sigmaC.

```
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 34 TPRVF 38

RESULT 3
Q8QV42
ID Q8QV42 PRELIMINARY; PRT; 51 AA.
AC Q8QV42;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL101 80M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL101 80M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354195; AAL83466.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 34 TPRVF 38

RESULT 4
Q8QV43
ID Q8QV43 PRELIMINARY; PRT; 51 AA.
AC Q8QV43;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL18 97M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL18 97M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354194; AAL83465.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 34 TPRVF 38

RESULT 5
Q8QV46
ID Q8QV46 PRELIMINARY; PRT; 51 AA.
AC Q8QV46;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL10 96M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL10 96M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354191; AAL83462.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 34 TPRVF 38

RESULT 6
Q8QV47
ID Q8QV47 PRELIMINARY; PRT; 51 AA.
AC Q8QV47;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL108 96M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177319;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL108 96M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354190; AAL83461.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 34 TPRVF 38
```

```

RESULT 7
Q8QV48      PRELIMINARY;      PRT;      51 AA.
ID Q8QV48;
AC Q8QV48;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL07 96M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177318;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL07 96M;
RA ter Huurne A.;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF354189; AAL83460.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
DB 34 TPRVF 38

RESULT 8
Q8QV51      PRELIMINARY;      PRT;      51 AA.
ID Q8QV51;
AC Q8QV51;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus NL07 97M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177315;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GEL08 97M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF354186; AAL83457.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
DB 34 TPRVF 38

RESULT 9
Q8QV52      PRELIMINARY;      PRT;      51 AA.
ID Q8QV52;
AC Q8QV52;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```

```

DE Sigma C protein (Fragment).
OS Avian reovirus GEL07 97M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GEL07 97M;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF354185; AAL83456.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0FE823ED41C0C4 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
DB 34 TPRVF 38

RESULT 10
Q8QV53      PRELIMINARY;      PRT;      51 AA.
ID Q8QV53;
AC Q8QV53;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus GEL04 97I.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GEL04 97I;
RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF354184; AAL83455.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1
FT NON_TER 51
SQ SEQUENCE 51 AA; 5632 MW; 4A0FE823ED57B1A3 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
DB 34 TPRVF 38

RESULT 11
Q8QV55      PRELIMINARY;      PRT;      51 AA.
ID Q8QV55;
AC Q8QV55;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sigma C protein (Fragment).
OS Avian reovirus GEI11 97M.
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=177311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GEI11 97M;

```

```

RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354182; AAL83453.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1 51
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0F823BD41C0C4 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 34 TPRVF 38

RESULT 12
Q88T47 ID Q88T47 PRELIMINARY; PRT; 91 AA.
AC Q88T47;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein lp_3141.
GN OrderedLocusNames=lp_3141.
OS Lactobacillus plantatum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935261; CAD65303.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 91 AA; 10638 MW; 15789F036EB55A9D CRC64;

Query Match 100.0%; Score 27; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 18 TPRVF 22

RESULT 13
Q6MNH8 ID Q6MNH8 PRELIMINARY; PRT; 97 AA.
AC Q6MNH8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transglycosylase associated protein.
GN OrderedLocusNames=Bdl276;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164;

RA Kant A., Balk F., Born L., van Roozelaar D., Heijmans J., Gielkens A.,
RA ter Huurne A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354182; AAL83453.1; -.
DR InterPro; IPR007662; Reo_sigmaC.
DR Pfam; PF04582; Reo_sigmaC; 1.
FT NON_TER 1 51
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 5660 MW; 4A0F823BD41C0C4 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 34 TPRVF 38

RESULT 12
Q88T47 ID Q88T47 PRELIMINARY; PRT; 91 AA.
AC Q88T47;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein lp_3141.
GN OrderedLocusNames=lp_3141.
OS Lactobacillus plantatum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935261; CAD65303.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 91 AA; 10638 MW; 15789F036EB55A9D CRC64;

Query Match 100.0%; Score 27; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 18 TPRVF 22

RESULT 13
Q6MNH8 ID Q6MNH8 PRELIMINARY; PRT; 97 AA.
AC Q6MNH8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transglycosylase associated protein.
GN OrderedLocusNames=Bdl276;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164;

RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842649; CAE79173.1; -.
DR InterPro; IPR007341; Transgly_assoc.
DR Pfam; PF04226; Transgly_assoc; 1.
KW Complete proteome.
SQ SEQUENCE 97 AA; 10712 MW; F3CB159308976941 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 60 TPRVF 64

RESULT 14
CAE79173 ID CAE79173 PRELIMINARY; PRT; 97 AA.
AC CAE79173;
DT 02-WAR-2004 (TrEMBLrel. 27, Created)
DT 02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Transglycosylase associated protein.
GN Bdl276.
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
DR EMBL; BX842649; CAE79173.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 97 AA; 10712 MW; F3CB159308976941 CRC64;

Query Match 100.0%; Score 27; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5
Db 60 TPRVF 64

RESULT 15
Q6LHW8 ID Q6LHW8 PRELIMINARY; PRT; 104 AA.
AC Q6LHW8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PPRBI240;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,

```

RA Valle G.;  
RT "Genome analysis of Photobacterium profundum reveals the complexity of  
RT high pressure adaptations.";  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR378678; CAG23112.1; -.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 104 AA; 11783 MW; 5679626687F6916E CRC64;

Query Match 100.0%; Score 27; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPRVF 5  
|||  
Db 86 TPRVF 90

Search completed: November 6, 2004, 19:52:56  
Job time : 69.875 secs

THIS PAGE BLANK (USPTO)

**THIS PAGE BLANK (USPTO)**